

145360

From: Sullivan, Daniel
Sent: Wednesday, February 16, 2005 1:37 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request 09754014

Please search for the following in the pending, issued patent and commercial databases:

A nucleic acid comprising SEQ ID NO: 10, 13, 17 or 19

Thank you

Daniel M. Sullivan

Examiner AU 1636
Remsen Bldg.
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 2/25/05
Date Completed: 3/2/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # 4
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 01
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:40:13 ; Search time 766.446 Seconds

(without alignments)
1042.930 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21
Sequence: 1 tttctttctctctctcmyag 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb_est3.*
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5: gb_est5.*
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7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	18.6	88.6	301	2	BB540713
3	18.6	88.6	327	2	BB125849
4	18.6	88.6	416	9	DR3213S
5	18.4	87.6	831	9	CC531199
6	18.4	85.7	347	4	B1402376
7	18.4	85.7	393	4	BG541755
8	18.4	85.7	409	2	AM785838
9	18.4	85.7	431	5	BK557861
10	18.4	85.7	482	5	B0874461
11	18.4	85.7	484	8	BX993189
12	18.4	85.7	500	9	CE507781
13	18.4	85.7	525	1	AJ682803
14	18.4	85.7	526	4	AQ174755
15	18.4	85.7	537	4	B1219527
16	18.4	85.7	539	8	B2277347
17	18.4	85.7	541	8	A0826373
18	18.4	85.7	557	9	CE518271
19	18.4	85.7	562	2	BE748929
20	18.4	85.7	575	9	CE569529
21	18.4	85.7	590	8	A2662964
22	18.4	85.7	605	8	AQ432329
23	18.4	85.7	614	8	A2443573
24	18.4	85.7	660	6	CB979909

25	18	85.7	661	8	CC433315
26	18	85.7	662	8	AZ034000
27	18	85.7	690	9	CE800232
28	18	85.7	727	8	AQ864238
29	18	85.7	727	8	BH933504
30	18	85.7	735	9	CL547365
31	18	85.7	739	9	AG414328
32	18	85.7	755	8	CC310172
33	18	85.7	756	2	BF792512
34	18	85.7	756	8	AQ914105
35	18	85.7	776	8	BH361022
36	18	85.7	791	8	CC366011
37	18	85.7	799	9	CC361830
38	18	85.7	810	8	AQ860653
39	18	85.7	811	4	BF966805
40	18	85.7	813	9	CC588569
41	18	85.7	827	5	BU359502
42	18	85.7	858	8	B2816652
43	18	85.7	866	8	AQ900621
44	18	85.7	894	9	CG363436
45	18	85.7	906	8	B2816655

ALIGNMENTS

RESULT 1
BG499610/c
LOCUS
DEFINITION
602546774F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669003 5',
mRNA sequence.

ACCESSION
BG499610
VERSION
BG499610.1
GI:13461127

KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 691)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov

COMMENT
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

High quality sequence stop: 211.
Location/Qualifiers
1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4669003"
/issue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccgcccggc); Site 2: SfiI
(ggcattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-AT(30)BN-3' (where B = A,
C, G, or T). Average insert size 1.5
kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,

FEATURES

source

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:04:23 ; Search time 110.385 Seconds
(without alignments)
1127.283 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21

Sequence: 1 tttctttctctctctcnyagg 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/ECTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19.6	93.3	160	17	US-10-400-053-7
5	19.6	93.3	160	17	US-10-419-045-13
6	19.6	93.3	3100	17	US-10-400-053-23
7	19.6	93.3	3558	18	US-10-281-067B-26
8	19.6	93.3	3558	18	US-10-764-818A-26
9	19.6	93.3	3589	15	US-10-234-406-1
10	19.6	93.3	3589	16	US-10-136-837-4
11	19.6	93.3	3609	15	US-10-234-406-3

12	19.6	93.3	4276	15	US-10-234-406-7	Sequence 7, Appli
13	19.6	93.3	4496	15	US-10-234-406-5	Sequence 5, Appli
14	19.6	93.3	4855	18	US-10-281-067B-27	Sequence 27, Appli
15	19.6	93.3	4855	18	US-10-764-818A-27	Sequence 27, Appli
16	19.6	93.3	5195	17	US-10-419-045-2	Sequence 2, Appli
17	19.6	93.3	5566	17	US-10-400-053-22	Sequence 22, Appli
18	19.6	93.3	5686	16	US-10-136-837-1	Sequence 1, Appli
19	19.6	93.3	5966	16	US-10-136-837-3	Sequence 3, Appli
20	18.6	88.6	362	17	US-10-632-117-23	Sequence 23, Appli
21	17.6	83.8	510	17	US-10-424-599-30471	Sequence 30471, A
22	17.6	83.8	921	17	US-10-335-977-4719	Sequence 4719, Ap
23	17.6	83.8	936	17	US-10-335-977-4720	Sequence 4720, Ap
24	17.6	83.8	201	19	US-10-741-600-25743	Sequence 25743, A
25	17.6	83.8	319	17	US-10-424-599-57372	Sequence 57372, A
26	17.6	83.8	321	18	US-10-767-701-28912	Sequence 28912, A
27	17.6	83.8	457	17	US-10-767-701-30036	Sequence 30036, A
28	17.6	83.8	464	13	US-10-027-632-40418	Sequence 40418, A
29	17.6	83.8	464	17	US-10-027-632-40418	Sequence 40418, A
30	17.6	83.8	468	10	US-09-918-995-29319	Sequence 29319, A
31	17.6	83.8	500	13	US-10-016-634A-92	Sequence 92, Appli
32	17.6	83.8	586	18	US-10-425-115-116190	Sequence 116190, A
33	17.6	83.8	627	18	US-10-357-930-53061	Sequence 53061, A
34	17.6	83.8	637	13	US-10-027-632-215696	Sequence 215696, A
35	17.6	83.8	637	17	US-10-027-632-215696	Sequence 215696, A
36	17.6	83.8	680	17	US-10-264-049-1938	Sequence 1938, Ap
37	17.6	83.8	713	17	US-10-424-599-127235	Sequence 127235, A
38	17.6	83.8	1044	9	US-09-938-842A-850	Sequence 850, App
39	17.6	83.8	1044	11	US-09-938-842A-850	Sequence 850, App
40	17.6	83.8	1145	9	US-09-984-245-99	Sequence 99, Appli
41	17.6	83.8	1145	10	US-09-966-262-89	Sequence 99, Appli
42	17.6	83.8	1145	10	US-09-983-966-89	Sequence 99, Appli
43	17.6	83.8	1145	14	US-10-059-395-99	Sequence 99, Appli
44	17.6	83.8	1145	14	US-10-143-090-99	Sequence 99, Appli
45	17.6	83.8	1147	13	US-10-087-192-1736	Sequence 1736, Ap

ALIGNMENTS

RESULT 1
US-09-754-014-10
Sequence 10, Application US/09754014
Patent No. US20020119940A1
GENERAL INFORMATION:
APPLICANT: Jeff No. US20020119940A1deltrcm
Bruce Freimark
Deena Deshpande
TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYSTEMS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Pasteo for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/754,014
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/948,958
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berkman, Charles S.

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:37:48 ; Search time 26.9231 seconds
(without alignments)
1276.296 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21

Sequence: 1 tctctctctctctctctcnyagsg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	17.6	83.8	601	4	US-09-949-016-26038
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5	17.6	83.8	601	4	US-09-949-016-74641
6	17.6	83.8	5599	2	US-08-477-451-9
7	17.6	83.8	5599	2	US-08-477-451-13
8	17.6	83.8	19932	2	US-08-477-451-25
9	17.6	83.8	92334	4	US-09-949-016-13920
10	17.6	83.8	92363	4	US-09-949-016-12146
11	17.6	83.8	601	4	US-09-949-016-22416
12	17.6	83.8	601	4	US-09-949-016-22417
13	17.6	83.8	601	4	US-09-949-016-153857
14	17.6	83.8	601	4	US-09-949-016-154221
15	17.6	83.8	601	4	US-09-949-016-154222
16	17.6	83.8	2431	4	US-09-023-655-810
17	17.6	83.8	3382	3	US-09-023-655-810
18	17.6	83.8	3382	3	US-09-023-655-810
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25	17.6	83.8	3382	3	US-09-023-655-810
26	17.6	83.8	3382	3	US-09-023-655-810
27	17.6	83.8	3382	3	US-09-023-655-810

28	17	81.0	55827	4	US-10-212-877-3	Sequence 3, Appl1
29	17	81.0	64813	4	US-09-949-016-11957	Sequence 11957, A
30	17	81.0	70131	4	US-09-949-016-16054	Sequence 16054, A
31	17	81.0	79824	4	US-09-949-016-13919	Sequence 13919, A
32	17	81.0	87594	4	US-09-949-016-12135	Sequence 12135, A
33	17	81.0	87611	4	US-09-949-016-16139	Sequence 16139, A
34	17	81.0	117001	4	US-09-949-016-15684	Sequence 15684, A
35	17	81.0	129658	4	US-09-949-016-17195	Sequence 17195, A
36	17	81.0	248968	4	US-09-949-016-12614	Sequence 12614, A
37	17	81.0	250958	4	US-09-949-016-16061	Sequence 16061, A
38	16.8	80.0	46698	4	US-09-949-016-17323	Sequence 17323, A
39	16.8	80.0	54382	4	US-09-949-016-12139	Sequence 12139, A
40	16.6	79.0	195	4	US-09-270-767-3604	Sequence 3604, Ap
41	16.6	79.0	195	4	US-09-270-767-3604	Sequence 18886, A
42	16.6	79.0	6728	4	US-09-949-016-13735	Sequence 13735, A
43	16.6	79.0	66480	4	US-09-949-016-14817	Sequence 14817, A
44	16.6	79.0	76563	4	US-09-949-016-17099	Sequence 17099, A
45	16.6	79.0	78269	4	US-09-949-016-12497	Sequence 12497, A

ALIGNMENTS

RESULT 1

US-09-012-366-7

Sequence 7, Application US/09012366

Patent No. 6034072

GENERAL INFORMATION:

APPLICANT: Robert Ralston

APPLICANT: Susanne Muller

APPLICANT: Ruse Mumper

APPLICANT: William Mungler

APPLICANT: Maria Bruno

TITLE OF INVENTION: IL-2 GENE EXPRESSION AND

DELIVERY SYSTEMS AND USES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/012,366

FILING DATE: January 23, 1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/039,709

FILING DATE: February 10, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Berkman, Charles S.

REGISTRATION NUMBER: 38,077

REFERENCE/DOCKET NUMBER: 230/214

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-012-366-7

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:30:33 ; Search time 91.7538 Seconds
(without alignments)

1354.870 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21
Sequence: 1 tctctctctctctctcnyagg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq.15Dec04:*
1: geneseq1808:*
2: geneseq1808:*
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4: geneseq2001a:*
5: geneseq2001b:*
6: geneseq2002a:*
7: geneseq2002b:*
8: geneseq2003a:*
9: geneseq2003b:*
10: geneseq2003c:*
11: geneseq2003d:*
12: geneseq2004a:*
13: geneseq2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.6	93.3	30	AAZ40413	Aaz40413 3' splice
2	19.6	93.3	30	ADP77253	Adp77253 Synthetic
3	19.6	93.3	45	AAV07276	Aav07276 Plasmid p
4	19.6	93.3	45	AAZ50395	Aaz50395 Synthetic
5	19.6	93.3	86	AAZ53801	Aaz53801 Intron #1
6	19.6	93.3	159	ADM94833	Adm94833 Synthetic
7	19.6	93.3	160	ABN86149	Abn86149 Nucleotide
8	19.6	93.3	160	ABQ74561	Abq74561 Synthetic
9	19.6	93.3	160	AAZ53803	Aaz53803 IVS8 DNA
10	19.6	93.3	1234	ADP97789	Adp97789 Human fcc
11	19.6	93.3	3026	10 AAD53819	Aad53819 PGHRH1674
12	19.6	93.3	3100	6 ABN86161	Abn86161 Nucleotide
13	19.6	93.3	3308	12 ADP77253	Adp77253 Human fcc
14	19.6	93.3	3323	12 ADP97788	Adp97788 Human fcc
15	19.6	93.3	3334	12 ADP97786	Adp97786 Human fcc
16	19.6	93.3	3558	9 AAL60457	Aal60457 pGRI174 p
17	19.6	93.3	3558	13 ADR23406	Adr23406 Inducible
18	19.6	93.3	3589	2 AAZ40418	Aaz40418 Plasmid p
19	19.6	93.3	3589	5 AAI70084	Aai70084 Plasmid p
20	19.6	93.3	3589	12 ADP77242	Adp77242 Human IFN

ALIGNMENTS

21	19.6	93.3	3609	5 AAI70085	Aai70085 Plasmid p
22	19.6	93.3	4276	5 AAI70087	Aai70087 Codon opt
23	19.6	93.3	4496	5 AAI70086	Aai70086 Plasmid p
24	19.6	93.3	4855	9 AAL60458	Aal60458 Nucleic-sp
25	19.6	93.3	4855	10 AAD53818	Aad53818 PGRI174 p
26	19.6	93.3	4855	13 ADR23407	Adr23407 Nucleic-sp
27	19.6	93.3	5195	6 ABQ74554	Abq74554 Human Del
28	19.6	93.3	5195	12 ADM94827	Adm94827 Human dev
29	19.6	93.3	5566	6 ABN86160	Abn86160 Nucleotide
30	19.6	93.3	5686	2 AAZ40415	Aaz40415 Plasmid p
31	19.6	93.3	5686	12 ADP77239	Adp77239 Human IL-
32	19.6	93.3	5966	2 AAZ40417	Aaz40417 Plasmid p
33	19.6	93.3	5966	12 ADP77241	Adp77241 Mouse IL-
34	18.6	88.6	362	6 ABS59810	Abs59810 Streptoco
35	17.6	83.8	495	3 AAC75463	Aac75463 Human ORF
36	17.6	83.8	19932	2 AAT46159	Aat46159 Cagl locu
37	17	81.0	201	13 ADS39455	Ads39455 Human aut
38	17	81.0	201	13 ADS38124	Ads38124 Human aut
39	17	81.0	468	9 ACH42107	Ach42107 Human fcc
40	17	81.0	500	8 ABV94001	Abv94001 Human COL
41	17	81.0	552	4 AAI12056	Aai12056 Human CDN
42	17	81.0	627	5 ABV53042	Abv53042 Human pro
43	17	81.0	680	6 ABQ56058	Abq56058 Human ova
44	17	81.0	778	5 AAB94487	Aab94487 Human fcc
45	17	81.0	1044	6 ABZ13045	Abz13045 Arabidops

RESULT 1
AAZ40413
ID AAZ40413 strand; DNA, 30 BP.
XX
AC AAZ40413;
XX
DT 15-FEB-2000 (first entry)
XX
DE 3' splice site sequence for interferon-alpha plasmid.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; intron; ss.
XX
OS Synthetic.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
(GENE-) GENEMEDICINE INC.
XX
Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
WPI, 1999-562116/47.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Disclosure; Page 31; 137pp; English.
XX
The invention relates to a novel plasmid comprising a cytomegalovirus
CC (CMV) promoter transcriptionally linked with an interferon alpha (IFN-
CC alpha) coding sequence, and a growth hormone 3'-untranslated region
CC (UTR). Sequences AAZ40412 and AAZ40413 represent synthetic 5' and 3'
CC splice donor and acceptor sites respectively for generating a synthetic
CC intron to be inserted into the plasmid of the invention. The plasmids can
CC be used for treating a mammalian condition or disease, particularly
CC cancer

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:40:13 ; Search time 255.482 Seconds
(without alignments)
1042.930 Million cell updates/sec

Title: US-09-754-014a-17

Perfect score: 7

Sequence: 1 taccac 7

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	19	7	CO786076
2	7	100.0	19	8	AZ623493
3	7	100.0	19	8	AZ778302
4	7	100.0	19	8	AZ806669
5	7	100.0	21	8	AZ812861
6	7	100.0	22	8	AZ851620
7	7	100.0	23	7	CF308058
8	7	100.0	23	8	AZ476882
9	7	100.0	23	9	AG189480
10	7	100.0	23	9	TA1646120
11	7	100.0	23	6	CD744129
12	7	100.0	24	8	AZ304717
13	7	100.0	25	8	BH910894
14	7	100.0	25	8	BZ381299
15	7	100.0	25	9	CG718650
16	7	100.0	25	9	CG718650
17	7	100.0	26	8	AZ364052
18	7	100.0	27	8	AZ351430
19	7	100.0	28	8	AZ609297
20	7	100.0	28	8	BH863505
21	7	100.0	28	9	AJ587873
22	7	100.0	29	8	BH910847
23	7	100.0	30	8	AZ480938
24	7	100.0	30	8	AZ480938

25	7	100.0	30	8	AZ591759
26	7	100.0	30	8	AZ857764
27	7	100.0	30	9	AL762304
28	7	100.0	30	9	DR19035
29	7	100.0	31	2	AV960314
30	7	100.0	31	2	AV960314
31	7	100.0	31	8	AZ318049
32	7	100.0	31	9	CG718776
33	7	100.0	32	8	AZ387853
34	7	100.0	32	8	AZ391582
35	7	100.0	32	8	AZ605009
36	7	100.0	32	8	BH852695
37	7	100.0	32	8	BH854186
38	7	100.0	32	8	BH904979
39	7	100.0	32	8	TA253H10P
40	7	100.0	33	8	AZ769247
41	7	100.0	33	8	BZ358044
42	7	100.0	33	9	AL766917
43	7	100.0	33	9	TA227D090
44	7	100.0	33	9	TA364B10P
45	7	100.0	34	1	AU256929

ALIGNMENTS

RESULT 1
LOCUS CO786076
DEFINITION BL285B E05 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
CDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION CO786076.1 GI:51002056
VERSION
KEYWORDS
SOURCE
ORGANISM Ambystoma mexicanum (axolotl)
Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroideae; Ambystomidae;
Ambystoma.
1 (bases 1 to 19)
Habermaun, B., Beblin, A.G., Herklotz, S., Volkmers, M., Eckel, K.,
Pelke, K., Epperlein, H.H., Schachert, H.K., Wiebe, G. and Tanaka, E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
Contact: Ely M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfeifferhauserstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL285B row: 05 column: E
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1..19
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
/note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unmutagenized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was poly(A) primed and cloned into
EMD108-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

ORIGIN

Query Match 100.0%; Score 7; DB 7; Length 19;

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:04:23 ; Search time 36.7949 Seconds
(without alignments)
1127.283 Million cell updates/sec

Title: US-09-754-014a-17

Perfect score: 7
Sequence: 1 tactaac 7

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	7	100.0	7	US-10-400-053-3	Sequence 3, Appl1
2	7	100.0	7	US-10-419-045-11	Sequence 11, Appl1
3	7	100.0	7	US-10-198-447A-24	Sequence 24, Appl1
4	7	100.0	7	US-10-333-914-6	Sequence 6, Appl1
5	7	100.0	7	US-10-374-784A-3	Sequence 3, Appl1
6	7	100.0	7	US-10-621-867-24	Sequence 24, Appl1
7	7	100.0	10	US-10-033-145-942	Sequence 942, App
8	7	100.0	10	US-10-225-501-3	Sequence 3, Appl1
9	7	100.0	11	US-10-149-109A-27	Sequence 27, Appl1
10	7	100.0	11	US-10-149-109A-28	Sequence 28, Appl1
11	7	100.0	12	US-10-257-017B-267651	Sequence 267651,

12	7	100.0	12	US-10-257-017B-267994	Sequence 267994,
13	7	100.0	12	US-10-257-017B-268138	Sequence 268138,
14	7	100.0	12	US-10-257-017B-268269	Sequence 268269,
15	7	100.0	12	US-10-257-017B-269417	Sequence 269417,
16	7	100.0	12	US-10-257-017B-269425	Sequence 269425,
17	7	100.0	12	US-10-257-017B-269953	Sequence 269953,
18	7	100.0	12	US-10-257-017B-270179	Sequence 270179,
19	7	100.0	12	US-10-257-017B-271344	Sequence 271344,
20	7	100.0	12	US-10-257-017B-271630	Sequence 271630,
21	7	100.0	12	US-10-257-017B-272883	Sequence 272883,
22	7	100.0	12	US-10-257-017B-272847	Sequence 272847,
23	7	100.0	12	US-10-257-017B-272997	Sequence 272997,
24	7	100.0	12	US-10-257-017B-274276	Sequence 274276,
25	7	100.0	12	US-10-257-017B-274934	Sequence 274934,
26	7	100.0	12	US-10-257-017B-275558	Sequence 275558,
27	7	100.0	12	US-10-257-017B-276558	Sequence 276558,
28	7	100.0	12	US-10-257-017B-276869	Sequence 276869,
29	7	100.0	12	US-10-257-017B-277250	Sequence 277250,
30	7	100.0	12	US-10-257-017B-277367	Sequence 277367,
31	7	100.0	12	US-10-257-017B-277368	Sequence 277368,
32	7	100.0	12	US-10-257-017B-277907	Sequence 277907,
33	7	100.0	12	US-10-257-017B-278347	Sequence 278347,
34	7	100.0	12	US-10-257-017B-278659	Sequence 278659,
35	7	100.0	12	US-10-257-017B-278660	Sequence 278660,
36	7	100.0	12	US-10-257-017B-278969	Sequence 278969,
37	7	100.0	12	US-10-257-017B-279336	Sequence 279336,
38	7	100.0	12	US-10-257-017B-279420	Sequence 279420,
39	7	100.0	12	US-10-257-017B-279421	Sequence 279421,
40	7	100.0	12	US-10-257-017B-279748	Sequence 279748,
41	7	100.0	12	US-10-257-017B-280030	Sequence 280030,
42	7	100.0	12	US-10-257-017B-280031	Sequence 280031,
43	7	100.0	12	US-10-257-017B-280219	Sequence 280219,
44	7	100.0	12	US-10-257-017B-280345	Sequence 280345,
45	7	100.0	12	US-10-257-017B-284147	Sequence 284147,

ALIGNMENTS

RESULT 1
US-10-400-053-3
Sequence 3, Application US/10400053
Publication No. US20030220286A1
GENERAL INFORMATION:
APPLICANT: Abnuzee, Ronald V
APPLICANT: Mehta, Vidya
APPLICANT: No. US20030220286A1dstrom, Jeffrey L
APPLICANT: Fewell, Jason
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Improved System for Regulation of Transgene Expression
FILE REFERENCE: 213-0080US
CURRENT APPLICATION NUMBER: US/10/400,053
PRIOR FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: PCT/US01/30305
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/260,781
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/278,281
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/235,030
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 3
LENGTH: 7
TYPES: RNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: branch point sequence for a synthetic intron
US-10-400-053-3
Query Match 100.0%; Score 7; DB 17; Length 7;

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:37:48 ; Search time 8.97436 Seconds
(without alignments)
1276.296 Million cell updates/sec

Title: US-09-754-014a-17

Perfect score: 7
Sequence: 1 taccac 7

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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5: /cgn2_6/prodata/1/ina/6C_COMB.seq:*
6: /cgn2_6/prodata/1/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	US-09-403-267-1	Sequence 1, Appli
2	7	100.0	7	US-09-349-740A-8	Sequence 8, Appli
3	7	100.0	9	US-08-646-789A-63	Sequence 63, Appli
4	7	100.0	12	US-08-607-078-5	Sequence 5, Appli
5	7	100.0	12	US-09-403-267-33	Sequence 33, Appli
6	7	100.0	12	US-09-359-921-5	Sequence 5, Appli
7	7	100.0	12	US-09-360-344-5	Sequence 5, Appli
8	7	100.0	13	US-08-148-058A-2	Sequence 2, Appli
9	7	100.0	13	US-08-478-042-2	Sequence 2, Appli
10	7	100.0	13	US-08-645-213-2	Sequence 2, Appli
11	7	100.0	13	US-08-466-604-2	Sequence 2, Appli
12	7	100.0	14	US-08-297-808A-4	Sequence 4, Appli
13	7	100.0	15	US-09-242-690A-16	Sequence 16, Appli
14	7	100.0	15	US-09-908-855-16	Sequence 16, Appli
15	7	100.0	16	US-09-731-466-4	Sequence 4, Appli
16	7	100.0	16	US-09-474-432B-3	Sequence 3, Appli
17	7	100.0	16	US-09-476-387-3	Sequence 3, Appli
18	7	100.0	16	US-09-476-387-3	Sequence 3, Appli
19	7	100.0	16	US-09-476-387-3	Sequence 3, Appli
20	7	100.0	17	US-07-990-965-3	Sequence 3, Appli
21	7	100.0	17	US-08-758-306-347	Sequence 347, App
22	7	100.0	17	US-08-758-306-349	Sequence 349, App
23	7	100.0	17	US-08-758-306-351	Sequence 351, App
24	7	100.0	17	US-08-758-306-1315	Sequence 1315, Ap
25	7	100.0	17	US-08-758-306-1317	Sequence 1317, Ap
26	7	100.0	17	US-08-758-306-1319	Sequence 1319, Ap
27	7	100.0	17	US-08-758-306-1321	Sequence 1321, Ap

28	7	100.0	17	US-09-731-466-5	Sequence 5, Appli
29	7	100.0	17	US-09-479-279-5	Sequence 5, Appli
30	7	100.0	17	US-09-479-279-5	Sequence 5, Appli
31	7	100.0	18	US-08-683-743-19	Sequence 19, Appli
32	7	100.0	18	US-08-810-559-65	Sequence 65, Appli
33	7	100.0	18	US-08-784-582-63	Sequence 63, Appli
34	7	100.0	18	US-08-413-740A-152	Sequence 152, App
35	7	100.0	18	US-09-334-938-20	Sequence 20, Appli
36	7	100.0	18	US-09-649-747A-50	Sequence 50, Appli
37	7	100.0	18	US-09-422-978-10632	Sequence 7208, Ap
38	7	100.0	18	US-09-422-978-10632	Sequence 10632, A
39	7	100.0	18	PCT-US95-04063-152	Sequence 152, App
40	7	100.0	19	US-08-219-842-24	Sequence 24, Appli
41	7	100.0	19	US-08-066-325-20	Sequence 20, Appli
42	7	100.0	19	US-08-451-096-24	Sequence 24, Appli
43	7	100.0	19	US-08-483-695-15	Sequence 15, Appli
44	7	100.0	19	US-07-965-285-15	Sequence 15, Appli
45	7	100.0	19	US-08-487-231-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-09-403-267-1
Sequence 1, Application US/09403267
Patent No. 6159710
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy, and Biology
APPLICANT: Fraser, Nigel W.
APPLICANT: Zabolotny, Janice M.
APPLICANT: Krumenacher, Claude F.
TITLE OF INVENTION: Method and Compositions for Stabilizing
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09403,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,664
FILING DATE: 18-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST78APCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9700
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: RNA (genomic)
US-09-403-267-1
Query Match 100.0%; Score 7; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.3e+08;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:30:33 ; Search time 30.5846 Seconds
(without alignments)
1354.870 Million cell updates/sec

Title: US-09-754-014A-17

Perfect score: 1 tctaac 7

Scoring table: IDENTITY NUC
dapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn19808:*

2: geneseqn19908:*

3: geneseqn20008:*

4: geneseqn20018:*

5: geneseqn20028:*

6: geneseqn20038:*

7: geneseqn20048:*

8: geneseqn20058:*

9: geneseqn20068:*

10: geneseqn20078:*

11: geneseqn20088:*

12: geneseqn20098:*

13: geneseqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	2	AAV43560 Insertion
2	7	100.0	7	2	AAV43552 Insertion
3	7	100.0	7	2	AAV43552 Insertion
4	7	100.0	7	2	AAV43552 Insertion
5	7	100.0	7	2	AAV43552 Insertion
6	7	100.0	7	2	AAV43552 Insertion
7	7	100.0	7	2	AAV43552 Insertion
8	7	100.0	7	2	AAV43552 Insertion
9	7	100.0	7	2	AAV43552 Insertion
10	7	100.0	7	2	AAV43552 Insertion
11	7	100.0	7	2	AAV43552 Insertion
12	7	100.0	7	2	AAV43552 Insertion
13	7	100.0	7	2	AAV43552 Insertion
14	7	100.0	7	2	AAV43552 Insertion
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16	7	100.0	7	2	AAV43552 Insertion
17	7	100.0	7	2	AAV43552 Insertion
18	7	100.0	7	2	AAV43552 Insertion
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20	7	100.0	7	2	AAV43552 Insertion

C	21	7	100.0	12	5	AB117485	Ab117485 Oligonucleotide
C	22	7	100.0	12	5	ABH68017	AbH68017 Oligonucleotide
C	23	7	100.0	12	5	ABH69440	AbH69440 Oligonucleotide
C	24	7	100.0	12	5	ABH95945	AbH95945 Oligonucleotide
C	25	7	100.0	12	5	ABH95945	AbH95945 Oligonucleotide
C	26	7	100.0	12	5	ABH98712	AbH98712 Oligonucleotide
C	27	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	28	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	29	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	30	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	31	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	32	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	33	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	34	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	35	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	36	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	37	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	38	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
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C	42	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	43	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	44	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide
C	45	7	100.0	12	5	ABH99910	AbH99910 Oligonucleotide

ALIGNMENTS

RESULT 1
AAV43560
ID AAV43560 standard; DNA; 7 BP.
XX
AC AAV43560;
XX
DT 25-MAR-2003 (revised)
DT 16-SEP-1998 (first entry)
XX
DE Insertion sequence 13 used for creating a tagged gene.
XX
OS Tagged gene; tagged transcript; hybrid fusion; protein tag;
XX protein isolation; recombination; subcellular structure analysis;
XX transcriptional regulation; viral infection; ss.
XX
OS Synthetic.
XX Unidentified.
XX
XX WO9820031-A1.
XX
XX 14-MAY-1998.
XX
PF 07-NOV-1997; 97WO-US020150.
XX
PR 08-NOV-1996; 96US-00745404.
XX
PA (JARV/) JARVIK J W.
XX
PI Jarvik JW;
XX
XX WPI; 1998-286661/25.
XX
PT Tagging genes, transcripts and proteins - using tag-creating DNA inserted
PT into fusion of gene to create 2 hybrid introns separated by new exon
PT encoding protein tag.
XX
PS Claim 1; Page 33; 66pp; English.
XX
CC This sequence is used in the method of invention for tagging genes,
CC transcripts and proteins in cells in a single recombinational event. The
CC method comprises producing a tagged gene by inserting a DNA sequence into
CC an intron of a gene by selecting a DNA sequence having a 5' portion free
CC of any nucleotide sequence selected from AAV43548 to AAV43551, a

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:35:38 ; Search time 115.626 Seconds
(without alignments)
2933.489 Million cell updates/sec

Title: US-09-754-014A-17

Perfect score: 1 tctaac 7

Sequence: 1 tctaac 7

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	7	100.0	7	6	AX451625 Sequence
3	7	100.0	8	6	AX770099 Sequence
4	7	100.0	10	6	BD239524 Sequence
5	7	100.0	11	6	AX175038 Sequence
6	7	100.0	11	6	AX175039 Sequence
7	7	100.0	12	6	AR121253 Sequence
8	7	100.0	12	6	AR305536 Sequence
9	7	100.0	12	6	AR455354 Sequence
10	7	100.0	13	6	AR037996 Sequence
11	7	100.0	13	6	AR039094 Sequence
12	7	100.0	13	6	AR050339 Sequence
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14	7	100.0	15	6	BD208263 Sequence
15	7	100.0	15	6	BD208264 Sequence
16	7	100.0	15	6	BD208265 Enzymatic
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18	7	100.0	15	6	AR382531 Enzymatic
19	7	100.0	15	6	AX587026 Sequence

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24	7	100.0	16	6	AR397623 Sequence
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31	7	100.0	17	6	AR040473 Sequence
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33	7	100.0	17	6	BD201648 Method an
34	7	100.0	17	6	BD201649 Method an
35	7	100.0	17	6	BD201650 Method an
36	7	100.0	17	6	E01964 DNA encodin
37	7	100.0	17	6	E03611 DNA primer
38	7	100.0	17	6	I26214 Sequence 3
39	7	100.0	17	6	AR211429 Sequence
40	7	100.0	17	6	AR213616 Sequence
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ALIGNMENTS

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VERSION	AX203149.1	GI:15392500				
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:04:23 ; Search time 641.282 Seconds
(without alignments)

1127.283 Million cell updates/sec

Title: us-09-754-014a-13

Perfect score: 122

Sequence: 1 ccgctgaagctctctctctctctctctctctctctctctcagag 122

Scoring table: 1IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	45	36.9	3589	15	US-10-234-406-1
5	45	36.9	3589	15	US-10-136-837-4
6	45	36.9	3609	15	US-10-234-406-3
7	45	36.9	4276	15	US-10-234-406-7
8	45	36.9	4496	15	US-10-234-406-5
9	45	36.9	4855	18	US-10-281-067B-27
10	45	36.9	4855	18	US-10-764-818A-27
11	45	36.9	5195	17	US-10-419-045-2

12	45	36.9	5566	17	US-10-400-053-22	Sequence 22, Appl
13	45	36.9	5586	16	US-10-136-837-1	Sequence 1, Appl
14	45	36.9	5596	16	US-10-136-837-3	Sequence 3, Appl
15	45	36.9	160	17	US-10-400-053-7	Sequence 7, Appl
16	34	27.9	160	17	US-10-419-045-13	Sequence 13, Appl
17	30	24.6	45	9	US-09-754-014-10	Sequence 10, Appl
18	30	24.6	45	9	US-09-836-866-6	Sequence 6, Appl
19	28	23.0	86	17	US-10-400-053-5	Sequence 5, Appl
20	26	21.3	1399	17	US-10-369-493-29964	Sequence 29964, A
21	25.4	20.8	201	18	US-10-719-993-30427	Sequence 30427, A
22	25.4	20.8	4602	10	US-09-809-391-74	Sequence 74, Appl
23	25.4	20.8	4602	10	US-09-882-171-74	Sequence 74, Appl
24	25.4	20.8	4602	17	US-10-164-861-74	Sequence 74, Appl
25	25.4	20.8	775062	18	US-10-719-993-6844	Sequence 6844, Ap
26	24.8	20.3	2318	18	US-10-357-930-28435	Sequence 28435, A
27	24.6	20.2	975	18	US-10-425-115-165294	Sequence 165294, A
28	24.6	20.2	2786	10	US-09-809-391-238	Sequence 238, App
29	24.6	20.2	2786	10	US-09-882-171-238	Sequence 238, App
30	24.6	20.2	2786	17	US-10-164-861-238	Sequence 238, App
31	24.6	20.2	2801	17	US-10-425-114-32778	Sequence 32778, A
32	24.6	20.2	3448	18	US-10-425-115-165295	Sequence 165295, A
33	24.4	20.0	1395	17	US-10-369-493-29963	Sequence 29963, A
34	24.4	19.7	32188	9	US-09-764-860-799	Sequence 799, App
35	24	19.7	32188	14	US-10-074-095-799	Sequence 799, App
36	24	19.7	32188	17	US-10-212-872-799	Sequence 799, App
37	24	19.7	180227	18	US-10-322-281-308	Sequence 308, App
38	23.8	19.5	2088	10	US-09-814-353-19402	Sequence 19402, A
39	23.8	19.5	344548	13	US-10-087-192-334	Sequence 334, App
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ALIGNMENTS

RESULT 1
US-10-400-053-23
Sequence 23, Application US/10400053
Publication No. US20030220286A1
GENERAL INFORMATION:
APPLICANT: Adizzeze, Ronald V
APPLICANT: Mehta, Vidya
APPLICANT: No. US20030220286A1dctrom, Jeffrey L
APPLICANT: Fowell, Jason
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Improved System for Regulation of Transgene Expression
FILE REFERENCE: 213-0080US
CURRENT APPLICATION NUMBER: US/10/400,053
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: PCT/US01/30305
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/260,781
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/278,281
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/235,030
PRIOR FILING DATE: 2000-09-25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 3100
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: Complete nucleic acid sequence of pP1666 plasmid.
US-10-400-053-23
Query Match 36.9%, Score 45, DB 17, Length 3100,

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:37:48 ; Search time 156.41 Seconds
(without alignments)
1276.296 Million cell updates/sec

Title: US-09-754-014A-13

Perfect score: 122
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	25.4	20.8	4602	US-09-149-476-74	Sequence 74, Appl
3	24.6	20.2	2786	US-09-149-476-238	Sequence 238, Appl
4	23.4	19.2	120609	US-09-949-016-13915	Sequence 13915, A
5	23.2	19.0	974	US-09-509-012B-4	Sequence 4, Appl
6	23	18.9	913	US-09-774-528-410	Sequence 410, Appl
7	23	18.9	264665	US-09-949-016-13747	Sequence 13747, A
8	22.8	18.7	1055	US-09-270-767-9711	Sequence 9711, Ap
9	22.8	18.7	1055	US-09-270-767-24993	Sequence 24993, A
10	22.6	18.5	970	US-09-509-012B-122	Sequence 122, Appl
11	22.6	18.5	988	US-09-509-012B-54	Sequence 54, Appl
12	22.4	18.4	4098	US-08-605-106-4	Sequence 4, Appl
13	22.4	18.4	189560	US-09-949-016-17202	Sequence 17202, A
14	22.2	18.2	544	US-09-490-818-2	Sequence 2, Appl
15	22.2	18.2	588	US-09-543-681A-127	Sequence 127, Appl
16	22.2	18.2	2860	US-09-221-017B-871	Sequence 871, Appl
17	22.2	18.2	22980	US-09-949-016-16145	Sequence 16145, A
18	22.2	18.2	245286	US-09-949-016-15497	Sequence 15497, A
19	22	18.0	601	US-09-949-016-146471	Sequence 146471, A
20	22	18.0	52821	US-09-949-016-15857	Sequence 15857, A
21	22	18.0	52824	US-09-949-016-12116	Sequence 12116, A
22	21.8	17.9	601	US-09-949-016-18015	Sequence 18015, A
23	21.8	17.9	601	US-09-949-016-51591	Sequence 51591, A
24	21.8	17.9	601	US-09-949-016-56814	Sequence 56814, A
25	21.8	17.9	601	US-09-949-016-56815	Sequence 56815, A
26	21.8	17.9	601	US-09-949-016-56816	Sequence 56816, A
27	21.8	17.9	601	US-09-949-016-56817	Sequence 56817, A

28	21.8	17.9	95621	US-09-949-016-13237	Sequence 13237, A
29	21.8	17.9	161124	US-09-949-016-11760	Sequence 11760, A
30	21.8	17.9	392000	US-10-027-983-11	Sequence 11, Appl
31	21.8	17.9	636591	US-09-949-016-11808	Sequence 11808, A
32	21.8	17.9	636591	US-09-949-016-13388	Sequence 13388, A
33	21.6	17.7	368	US-09-513-999C-24491	Sequence 24491, A
34	21.6	17.7	601	US-09-949-016-172289	Sequence 172289, A
35	21.6	17.7	79888	US-09-949-016-13274	Sequence 1274, A
36	21.6	17.7	79889	US-09-949-016-16254	Sequence 16254, A
37	21.6	17.7	106929	US-09-949-016-12060	Sequence 12060, A
38	21.6	17.7	106929	US-09-949-016-16618	Sequence 16618, A
39	21.6	17.7	155617	US-09-949-016-16191	Sequence 16191, A
40	21.6	17.7	254405	US-09-949-016-14381	Sequence 14381, A
41	21.4	17.5	601	US-09-949-016-179238	Sequence 179238, A
42	21.4	17.5	601	US-09-949-016-190619	Sequence 190619, A
43	21.4	17.5	2418	US-09-107-532A-2849	Sequence 2849, Ap
44	21.4	17.5	107937	US-09-949-016-17192	Sequence 17192, A
45	21.4	17.5	177293	US-09-949-016-16513	Sequence 16513, A

ALIGNMENTS

RESULT 1
US-09-012-366-7

Sequence 7, Application US/09012366
Patent No. 6034072

GENERAL INFORMATION:

APPLICANT: Robert Palston
APPLICANT: Susanne Muller

APPLICANT: Russ Munger
APPLICANT: William Munger

APPLICANT: Maria Bruno
TITLE OF INVENTION: IL-2 GENE EXPRESSION AND

TITLE OF INVENTION: DELIVERY SYSTEMS AND
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street

STREET: Suite 4700
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage

OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,366

FILING DATE: January 23, 1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/039,709

FILING DATE: February 10, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Berkman, Charles S.
REGISTRATION NUMBER: 38,077

REFERENCE/DOCKET NUMBER: 230/214
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ. ID NO. 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-09-012-366-7

Q854738

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: March 1, 2005, 12:40:13 ; Search time 1642.38 Seconds
(without alignments)
1042.930 Million cell updates/sec

Title: US-09-754-014a-10

Perfect score: 45
Sequence: 1 caggttaagtgctctcacta.....tcttttctctcaccag 45

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gseq1:
9: gb_gseq2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29.8	66.2	195	1	AL967706
2	29.8	66.2	717	7	CN094522 EC2BA9DF
3	29.8	66.2	869	5	BX777470
4	29.8	66.2	914	7	CR567097
5	26	57.8	750	8	BZ061605
6	25.6	56.9	944	9	CL087908
7	25	55.6	377	4	BG956291
8	25	55.6	608	5	BQ633133
9	25	55.6	722	1	AJ813585
10	24.8	55.1	282	2	BB719536
11	24.8	55.1	410	9	CE408506
12	24.8	55.1	417	1	AL653017
13	24.6	54.7	368	1	AV838611
14	24.6	54.7	387	1	AV948860
15	24.6	54.7	544	5	BM174638
16	24.6	54.7	550	5	BM303928
17	24.6	54.7	565	2	BF367918
18	24.6	54.7	603	1	AV858590
19	24.6	54.7	635	8	AZ405316
20	24.6	54.7	678	1	AV843858
21	24.6	54.7	682	5	BM158158
22	24.6	54.7	698	5	BM179050
23	24.6	54.7	698	5	BM269093
24	24.6	54.7	698	5	BM290068

25	24.6	54.7	746	5	BM180524
26	24.6	54.7	748	5	BM424520
27	24.6	54.7	750	5	BM419912
28	24.6	54.7	756	5	BM139250
29	24.6	54.7	761	5	BM085301
30	24.6	54.7	773	5	BM153823
31	24.6	54.7	777	5	BM160591
32	24.6	54.7	779	5	BM498931
33	24.6	54.7	1060	8	BZ261009
34	24.4	54.2	777	8	AQ748835
35	24.4	53.8	511	9	CG910690
36	24.2	53.8	603	9	CC695235
37	24.2	53.8	667	9	CE241851
38	24.2	53.8	682	8	AQ855610
39	24.2	53.8	710	5	BU337185
40	24.2	53.8	712	9	CC490080
41	24.2	53.8	890	8	AZ674043
42	24.2	53.8	919	6	CD362421
43	24.2	53.8	1141	8	CC290462
44	24	53.3	432	1	A1378640
45	24	53.3	506	8	BH777970

ALIGNMENTS

RESULT 1
LOCUS AL967706 195 bp mRNA linear EST 05-DEC-2003
DEFINITION XGC-gastrula Xenopus tropicalis cDNA clone Tgaal39m13 5',
AL967706
VERSION AL967706.2 GI:39023831
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 195)
Crotting, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Nov 27, 2002 this sequence version replaced gi:25791301.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tgaal39m13.p1kSPe
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13
gastrulae. EcoRI-NotI cut cDNA was then ligated into pcsl07 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pcsl07, Site 1: EcoRI, Site 2: NotI
Host: Escherichia coli XL1-blue.
location/Qualifiers
1..195
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/mol_type="mRNA"
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/dev_stage="gastrula (stages 10-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pcsl07, Site 1: EcoRI, Site 2: NotI, cDNA
was oligo dt primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pcsl07 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN

Query Match	100.0%;	Score 45;	DB 6;	Length 45;
Best Local Similarity	100.0%;	Pred. No. 0.00071;		
Matches 45;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:30:33 ; Search time 196.615 Seconds
(without alignments)
1354.870 Million cell updates/sec

Title: US-09-754-014A-10

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001a:*
5: geneeqn2001b:*
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7: geneeqn2002b:*
8: geneeqn2003a:*
9: geneeqn2003b:*
10: geneeqn2003c:*
11: geneeqn2003d:*
12: geneeqn2004a:*
13: geneeqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	45	2 AAV07276	AAV07276 Plasmid p
2	45	100.0	45	3 AAZ50395	Aaz50395 Synthetic
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4	31.4	69.8	160	6 ABQ74561	Abq74561 Synthetic
5	31.4	69.8	160	10 AAD53803	Aad53803 IVS8 DNA
6	31.4	69.8	5686	2 AAZ40415	Aaz40415 Plasmid p
7	31.4	69.8	5686	12 ADF77239	Adf77239 Human IL-
8	30	66.7	30	2 AAZ40413	Aaz40413 3' splice
9	30	66.7	30	12 ADF77253	Adf77253 Synthetic
10	30	66.7	3026	10 AAD53819	Aad53819 pGEMH1.674
11	30	66.7	3100	6 ABN86161	Abn86161 Nucleoid
12	30	66.7	3308	12 ABQ74561	Abq74561 Human fcc
13	30	66.7	3323	12 ADF77253	Adf77253 Human fcc
14	30	66.7	3334	12 ADF77253	Adf77253 Human fcc
15	30	66.7	3358	12 ADF77253	Adf77253 Human fcc
16	30	66.7	3358	12 ADF77253	Adf77253 Human fcc
17	30	66.7	3358	12 ADF77253	Adf77253 Human fcc
18	30	66.7	3358	12 ADF77253	Adf77253 Human fcc
19	30	66.7	3358	12 ADF77253	Adf77253 Human fcc
20	30	66.7	3358	12 ADF77253	Adf77253 Human fcc

21	30	66.7	4276	5 AAI70087	AAI70087 Codon Opt
22	30	66.7	4496	5 AAI70086	AAI70086 Plasmid p
23	30	66.7	4855	9 AAL60458	Aal60458 Muscle-sp
24	30	66.7	4855	10 AAD53818	Aad53818 PCS1633 p
25	30	66.7	4855	13 ADR23407	Adr23407 Muscle-sp
26	30	66.7	5195	6 ABQ74554	Abq74554 Human Del
27	30	66.7	5195	12 ADM94827	Adm94827 Human dev
28	30	66.7	5566	2 ABN86160	Abn86160 Nucleoid
29	30	66.7	5966	2 AAZ40417	Aaz40417 Plasmid p
30	30	66.7	5966	12 ADF77241	Adf77241 Mouse IL-
31	28	62.2	86	10 AAD53801	Aad53801 Intron #1
32	25	55.6	159	12 ADM94833	Adm94833 Synthetic
33	24.6	54.7	1112	12 ADQ08637	Adq08637 Clona int
34	24.4	54.2	28564	10 ADP47140	Adp47140 Human gen
35	24	53.3	1234	12 ADL97789	Adl97789 Human fcc
36	23.8	52.9	2283	6 ABQ3434	Abq3434 Human CDN
37	23.6	52.4	110000	2 AAV21209_07	AAV21209_07 of
38	23.6	52.4	110000	2 AAV21209_08	AAV21209_08 of
39	23.2	51.6	1018	10 ADC86628	Adc86628 Human GPC
40	23.2	51.6	1018	10 ADC86756	Adc86756 Human gen
41	23	51.1	2356	10 ADE59119	Ades9119 Human gen
42	23	51.1	125322	13 ABD33622	Abd33622 Murine ca
43	23	51.1	263744	10 ADF08271	Adf08271 Mouse apo
44	22.8	50.7	50000	6 AAD26437	Aad26437 Human GRM
45	22.8	50.7	50000	6 AAD26400	Aad26400 Human glt

ALIGNMENTS

RESULT 1	AAV07276	standard; DNA; 45 BP.
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AC	AAV07276	
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DT	25-SRP-1998	(first entry)
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DE	Plasmid pIN0773 Intron.	
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KM	IL-12 subunit; expression construct; treatment: asthma;	
KW	microbial infection; viral infection; cancer; Human; Interleukin; ss.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
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FT	misc_feature	16..22
FT		/*tag= c
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FT		/*tag= d
FT		/note= "3' splice site"
PN	MO9817689-42.	
XX		
PD	30-APR-1998.	
XX		
PR	10-OCT-1997; 97NO-US018719.	
XX		
PR	18-OCT-1996; 96US-0028616r.	
XX		
PR	(GENE-) GENEMEDICINE INC.	
XX		
PR	Notation 3, Pictmark B, Designdable D,	
XX		
DR	WEI, 1998-261428173.	
XX		

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OM nucleic - nucleic search, using SW model

Run on: March 1, 2005, 13:37:48 ; Search time 57.6923 Seconds
(without alignments)
1276.236 Million cell updates/sec

Title: US-09-754-014A-10

Perfect score: 45
Sequence: 1 caggragagctctctcactca.....tctctctctctcagcag 45

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A COMB.seq.*
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3: /cgn2_6/prodata/1/ina/5A COMB.seq.*
4: /cgn2_6/prodata/1/ina/5B COMB.seq.*
5: /cgn2_6/prodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	30	66.7	30	3	US-09-012-366-7		Sequence 7, Appl
2	25.4	56.4	248968	4	US-09-949-016-12614		Sequence 12614, A
3	25.4	56.4	250958	4	US-09-949-016-16061		Sequence 16061, A
4	23.8	52.9	601	4	US-09-949-016-189815		Sequence 189815, A
5	23.8	52.9	601	4	US-09-949-016-189816		Sequence 189816, A
6	23.6	52.4	166476	4	US-09-949-016-17175		Sequence 17175, A
7	23.6	52.4	166476	4	US-08-916-421B-1		Sequence 1, Appl
8	23.6	52.4	166476	4	US-08-916-421B-1		Sequence 1, Appl
9	23.6	52.4	166476	4	US-08-916-421B-1		Sequence 1, Appl
10	22.4	49.8	69062	4	US-09-949-016-13608		Sequence 13608, A
11	22.4	49.8	69062	4	US-09-949-016-13609		Sequence 13609, A
12	22.4	49.8	69062	4	US-09-949-016-13610		Sequence 13610, A
13	22.2	49.3	1125	3	US-09-436-983-2		Sequence 2, Appl
14	22.2	49.3	1125	3	US-09-436-983-2		Sequence 2, Appl
15	22.2	49.3	1125	3	US-09-436-983-2		Sequence 2, Appl
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17	22.2	49.3	1125	3	US-09-436-983-2		Sequence 2, Appl
18	22.2	49.3	1125	3	US-09-436-983-2		Sequence 2, Appl
19	22.2	49.3	1125	3	US-09-436-983-2		Sequence 2, Appl
20	22.2	49.3	1125	3	US-09-436-983-2		Sequence 2, Appl
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22	21.8	48.4	315	4	US-09-248-796A-12307		Sequence 12307, A
23	21.8	48.4	315	4	US-09-248-796A-12307		Sequence 12307, A
24	21.8	48.4	315	4	US-09-248-796A-12307		Sequence 12307, A
25	21.8	48.4	315	4	US-09-248-796A-12307		Sequence 12307, A
26	21.8	48.4	315	4	US-09-248-796A-12307		Sequence 12307, A
27	21.8	48.4	315	4	US-09-248-796A-12307		Sequence 12307, A

28	21.8	48.4	58829	4	US-09-949-016-13146		Sequence 13146, A
29	21.8	48.4	87305	4	US-09-949-016-13430		Sequence 13430, A
30	21.8	48.4	87352	4	US-09-949-016-12053		Sequence 12053, A
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37	21.6	48.0	601	4	US-09-949-016-125940		Sequence 125940, A
38	21.6	48.0	601	4	US-09-949-016-155936		Sequence 155936, A
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42	21.6	48.0	28494	4	US-09-949-016-13200		Sequence 13200, A
43	21.6	48.0	47818	4	US-09-949-016-12324		Sequence 12324, A
44	21.6	48.0	48480	4	US-09-949-016-15166		Sequence 15166, A
45	21.6	48.0	57638	4	US-09-949-016-17000		Sequence 17000, A

ALIGNMENTS

RESULT 1
US-09-012-366-7
Sequence 7, Application US/09012366
Patent No. 6034072
GENERAL INFORMATION:
APPLICANT: Robert Ralston
APPLICANT: Susanne Muller
APPLICANT: Russ Mumper
APPLICANT: William Mumper
APPLICANT: Maria Bruno
TITLE OF INVENTION: IL-2 GENE EXPRESSION AND
TITLE OF INVENTION: DELIVERY SYSTEMS AND USRS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,366
FILING DATE: January 23, 1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/039,709
FILING DATE: February 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Berkman, Charles S.
REGISTRATION NUMBER: 38,077
REFERENCE/DOCKET NUMBER: 230/214
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO. 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-012-366-7